



IFW16

RAW SEQUENCE LISTING

DATE: 08/23/2004

PATENT APPLICATION: US/10/603,260A

TIME: 10:28:28

Input Set : A:\amended Sequence Listing.txt

Output Set: N:\CRF4\08232004\J603260A.raw

3 <110> APPLICANT: CJ Corporation

5 <120> TITLE OF INVENTION: An alkaline lipase from *Vibrio metschnikovii* RH530 and a

6 nucleotide sequence encoding the same

C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/603,260A

C--> 8 <141> CURRENT FILING DATE: 2003-06-24

W--> 0 <130> FILE REFERENCE:

8 <160> NUMBER OF SEQ ID NOS: 7

10 <170> SOFTWARE: KopatentIn 1.71

12 <210> SEQ ID NO: 1

13 <211> LENGTH: 2578

14 <212> TYPE: DNA

15 <213> ORGANISM: *Vibrio metschnikovii* RH530

17 <400> SEQUENCE: 1

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20	gcggcggtcta	cgtacttcag	agattaaggc	catgactagc	gtttcatata	aaatggtgtc	120
22	tcgccacgta	ccttgaatgg	cgatacgagc	ctggcggttg	ccctcttgct	tgaggatccc	180
24	gatttcaatt	tgcgcgatcg	gttgaaaatg	gaaatagcgt	aatgactgta	aaaaagtacg	240
26	attcaaatga	ggtgcatgct	gctctaaata	aacaatgtcg	gcacccgaaa	agcgcaatga	300
28	agccaactga	ttgatttctt	ggcgacttct	ctctaataaa	tcgctaattg	cttcatcact	360
30	gcgcacaatc	aattcatagc	gcacctcaac	atccggatag	aacgaatgaa	cggcctgcat	420
32	catattgatt	ttataggcat	caagatccaa	taaaactgcg	ataaaaaagag	gagaaaatag	480
34	gcgatcgctc	atgatgatgc	catcctttcg	ttcggtttca	ttcagtcatt	acgttagtaa	540
36	caacgtgttg	ctaacttttg	gcgaacaata	aagtaccctt	gtaagtttgt	caacttttgt	600
38	gacaaacctc	ctcagtcggt	atttggcctt	attataatta	tggatattga	ggggtaagga	660
40	cgtagtcata	acaacaatta	cagtaactct	gttatctgag	ttatgtttgt	cacaaagtct	720
42	tattttacatt	tgaccatcat	catgcactta	cctaaaataa	gcccggtgtt	tatttagggaa	780
44	gccattatga	ttgtcactat	cgatatgatt	tgtctgcgtc	ttgcgcgcaa	atctatccag	840
46	gtttttactgg	tgaaacgctc	taatccaaat	cggccagatt	gtggtaaatg	ggcattgctt	900
48	ggcgggatag	tgtatgacga	agatatgacc	gctcatggtg	gagaacctgt	cgatgaggat	960
50	tttgatgcag	cgagacgacg	tatttgcggt	caaaaagtcc	atacttatcc	taattttatc	1020
52	agcgatccgc	tgggtgatgg	caacccccaa	cgcgatccga	atggttggag	tgtcagtatt	1080
54	tcccattacg	ctttattaaa	cccgtggaat	gtcaaacaaa	tagaagattt	tggatcgac	1140
56	cccgcgcgcg	ctaattgggt	tgatcttcat	actttactca	aagaagaaat	gccgctggct	1200
58	tttgatcatg	tcgcgcgaaat	tcagcatgcg	tggcaaaaat	tacgcgctgc	ggttgaatac	1260
60	acatccgtgg	tactattttc	attagaaaaa	gagtttttag	tggcggtatg	tattgatgcc	1320
62	tacgccaaat	ttggcgctcg	agttaatcgc	atgaccatta	aacgcgcgtt	gatcaatacc	1380
64	ggggtgatcg	tcagtaccaa	taaaatggcc	gcaccttgta	aaggcaagg	agccaaacca	1440
66	gccaccgttt	atcgtcttgc	cagtcatgaa	gtcacctatt	ttcaaacctg	tttacgaggt	1500
68	taactgttgc	aaaactcgtg	acagtagggt	atgatgtcaa	ttgatgatag	gtaggaagca	1560
70	atgcagatta	ttcttgttca	tggactctat	atgcatggct	tggtaatgca	tccgcttagt	1620
72	catcgctctg	ataaaattgg	ttatcgctac	caaaccatta	gctacaactc	actcgctatc	1680
74	gatgatgagg	ccatttttgc	ccgccttgac	cgatcgctca	ctcatgcctc	gcctaagtgt	1740
76	ttagtcggac	acagtttggg	cggattgggt	atcaaactgt	atctagaatc	gcgcgcacgc	1800



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78 tcctgtgaaa ccctctccca tgtcgctgcc atcggtcac ctttgcaagg agcttccatt      1860
80 gtcaataaaa ttgagcaatt aggtttagggtgtggcactag gtaattcagc agaatttggg      1920
82 ttaaaagaac acgacgacga atcccgtat ccacaaaaat caggcagtat tgcaggaacg      1980
84 ataccttttag ggctgocgag ccttttactg cgcgatccac tggactccga tggtagcgtc      2040
86 acagtagaag aaacaaaaat agctggcatg acagatcata tcgcgatatc caccacttca      2100
88 tacgagaatg ctgtttaatc attccgttgc cgagcaaatc gaccactttc ttcgttatga      2160
90 ccgcttccgg cgctaaagcc gtttaaactt cagatgatag tgtacttcgt atcaaaccga      2220
92 tggtgattga aaacataccc accattcatt cagaataaga cgttgccatc atcagagctt      2280
94 tccccgcaa taaacaatcc gcgactttac gtctggccgc tttactaaa ttggcaagtgt      2340
96 tctgcgcgca tacgctgatg ccgcatagtt aagccagccc cgacaccgc caacaccgc      2400
98 tgacgcgccc tgacgggctt gtctgtctcc ggcattccgt tacagacaag ctgtgaccgt      2460
100 ctccgggagc tgcattgtgc agaggttttc accgtcatca ccgaaacgcg cgagacgaaa      2520
102 gggcctcgtg atacgcctat ttttataggt taatgtcatg ataataatgg tttcttag      2578
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 798
107 <212> TYPE: DNA
108 <213> ORGANISM: Vibrio metschnikovii RH530
110 <220> FEATURE:
111 <221> NAME/KEY: CDS
112 <222> LOCATION: (1)..(798)
113 <223> OTHER INFORMATION: valL1 gene
116 <400> SEQUENCE: 2
117 atg ttt gtc aca aag tct tat tta cat ttg acc atc atc atg cac tta      48
118 Met Phe Val Thr Lys Ser Tyr Leu His Leu Thr Ile Ile Met His Leu
119 1 5 10 15
121 cct aaa ata agc ccg ttg ttt att agg gaa gcc att atg att gtc act      96
122 Pro Lys Ile Ser Pro Leu Phe Ile Arg Glu Ala Ile Met Ile Val Thr
123 20 25 30
125 atc gat atg att tgt ctg cgt ctt gcg ccg aaa tct atc cag gtt tta      144
126 Ile Asp Met Ile Cys Leu Arg Leu Ala Pro Lys Ser Ile Gln Val Leu
127 35 40 45
129 ctg gtg aaa cgc tct aat cca aat ccg cca gat tgt ggt aaa tgg gca      192
130 Leu Val Lys Arg Ser Asn Pro Asn Arg Pro Asp Cys Gly Lys Trp Ala
131 50 55 60
133 ttg cct ggc ggg ata gtg tat gac gaa gat atg acc gct cat ggt gga      240
134 Leu Pro Gly Gly Ile Val Tyr Asp Glu Asp Met Thr Ala His Gly Gly
135 65 70 75 80
137 gaa cct gtc gat gag gat ttt gat gca gcg aga cga cgt att tgt cgg      288
138 Glu Pro Val Asp Glu Asp Phe Asp Ala Ala Arg Arg Arg Ile Cys Arg
139 85 90 95
141 caa aaa gtc cat act tat cct aat ttt atc agc gat ccg ctg gtt gat      336
142 Gln Lys Val His Thr Tyr Pro Asn Phe Ile Ser Asp Pro Leu Val Asp
143 100 105 110
145 ggc aac ccc aaa cgc gat ccg aat ggt tgg agt gtc agt att tcc cat      384
146 Gly Asn Pro Lys Arg Asp Pro Asn Gly Trp Ser Val Ser Ile Ser His
147 115 120 125
149 tac gct tta tta aac ccg tgg aat gtc aaa caa ata gaa gat ttt ggt      432
150 Tyr Ala Leu Leu Asn Pro Trp Asn Val Lys Gln Ile Glu Asp Phe Gly
151 130 135 140

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153 atc gac ccc gag cgc gct aat tgg ttt gat ctt cat act tta ctc aaa      480
154 Ile Asp Pro Glu Arg Ala Asn Trp Phe Asp Leu His Thr Leu Leu Lys
155 145                      150                      155                      160
157 gaa gaa atg ccg ctg gct ttt gat cat gtc gcg caa att cag cat gcg      528
158 Glu Glu Met Pro Leu Ala Phe Asp His Val Ala Gln Ile Gln His Ala
159                      165                      170                      175
161 tgg caa aaa tta cgc gct gcg gtt gaa tac aca tcc gtg gta cta ttt      576
162 Trp Gln Lys Leu Arg Ala Ala Val Glu Tyr Thr Ser Val Val Leu Phe
163                      180                      185                      190
165 tca tta gaa aaa gag ttt tta gtg gcg gat att att gat gcc tac gcc      624
166 Ser Leu Glu Lys Glu Phe Leu Val Ala Asp Ile Ile Asp Ala Tyr Ala
167                      195                      200                      205
169 aaa ttt ggc gtc gaa gtt aat cgc atg acc att aaa cgc cgc ttg atc      672
170 Lys Phe Gly Val Glu Val Asn Arg Met Thr Ile Lys Arg Arg Leu Ile
171                      210                      215                      220
173 aat acc ggg gtg atc gtc agt acc aat aaa atg gcc gca tct tgt aaa      720
174 Asn Thr Gly Val Ile Val Ser Thr Asn Lys Met Ala Ala Ser Cys Lys
175 225                      230                      235                      240
177 ggc aaa gga gcc aaa cca gcc acc gtt tat cgt ctt gcc agt cat gaa      768
178 Gly Lys Gly Ala Lys Pro Ala Thr Val Tyr Arg Leu Ala Ser His Glu
179                      245                      250                      255
181 gtc acc tat ttt caa acc tgt tta cga ggt      798
182 Val Thr Tyr Phe Gln Thr Cys Leu Arg Gly
183                      260                      265
186 <210> SEQ ID NO: 3
187 <211> LENGTH: 266
188 <212> TYPE: PRT
189 <213> ORGANISM: Vibrio metschnikovii RH530
191 <400> SEQUENCE: 3
192 Met Phe Val Thr Lys Ser Tyr Leu His Leu Thr Ile Ile Met His Leu
193 1 5 10 15
195 Pro Lys Ile Ser Pro Leu Phe Ile Arg Glu Ala Ile Met Ile Val Thr
196 20 25 30
198 Ile Asp Met Ile Cys Leu Arg Leu Ala Pro Lys Ser Ile Gln Val Leu
199 35 40 45
201 Leu Val Lys Arg Ser Asn Pro Asn Arg Pro Asp Cys Gly Lys Trp Ala
202 50 55 60
204 Leu Pro Gly Gly Ile Val Tyr Asp Glu Asp Met Thr Ala His Gly Gly
205 65 70 75 80
207 Glu Pro Val Asp Glu Asp Phe Asp Ala Ala Arg Arg Arg Ile Cys Arg
208 85 90 95
210 Gln Lys Val His Thr Tyr Pro Asn Phe Ile Ser Asp Pro Leu Val Asp
211 100 105 110
213 Gly Asn Pro Lys Arg Asp Pro Asn Gly Trp Ser Val Ser Ile Ser His
214 115 120 125
216 Tyr Ala Leu Leu Asn Pro Trp Asn Val Lys Gln Ile Glu Asp Phe Gly
217 130 135 140
219 Ile Asp Pro Glu Arg Ala Asn Trp Phe Asp Leu His Thr Leu Leu Lys
220 145 150 155 160

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222 Glu Glu Met Pro Leu Ala Phe Asp His Val Ala Gln Ile Gln His Ala
223           165                      170                      175
225 Trp Gln Lys Leu Arg Ala Ala Val Glu Tyr Thr Ser Val Val Leu Phe
226           180                      185                      190
228 Ser Leu Glu Lys Glu Phe Leu Val Ala Asp Ile Ile Asp Ala Tyr Ala
229           195                      200                      205
231 Lys Phe Gly Val Glu Val Asn Arg Met Thr Ile Lys Arg Arg Leu Ile
232           210                      215                      220
234 Asn Thr Gly Val Ile Val Ser Thr Asn Lys Met Ala Ala Ser Cys Lys
235 225           230                      235                      240
237 Gly Lys Gly Ala Lys Pro Ala Thr Val Tyr Arg Leu Ala Ser His Glu
238           245                      250                      255
240 Val Thr Tyr Phe Gln Thr Cys Leu Arg Gly
241           260                      265
244 <210> SEQ ID NO: 4
245 <211> LENGTH: 555
246 <212> TYPE: DNA
247 <213> ORGANISM: Vibrio metschnikovii RH530
249 <220> FEATURE:
250 <221> NAME/KEY: CDS
251 <222> LOCATION: (1)..(555)
252 <223> OTHER INFORMATION: valL2 gene
255 <400> SEQUENCE: 4
256 atg cag att att ctt gtt cat gga ctc tat atg cat ggc ttg gta atg      48
257 Met Gln Ile Ile Leu Val His Gly Leu Tyr Met His Gly Leu Val Met
258 1           5           10           15
260 cat ccg ctt agt cat cgt ctg cat aaa ttg ggt tat cgt act caa acc      96
261 His Pro Leu Ser His Arg Leu His Lys Leu Gly Tyr Arg Thr Gln Thr
262           20           25           30
264 att agc tac aac tca ctc gct atc gat gat gag gcc att ttt cgc cgc      144
265 Ile Ser Tyr Asn Ser Leu Ala Ile Asp Asp Glu Ala Ile Phe Arg Arg
266           35           40           45
268 ctt gac cga tcg ctc act cat gcc tcg cct aat gct tta gtc gga cac      192
269 Leu Asp Arg Ser Leu Thr His Ala Ser Pro Asn Ala Leu Val Gly His
270           50           55           60
272 agt ttg ggc gga ttg gtg atc aaa cgt tat cta gaa tcg cgc gca ccg      240
273 Ser Leu Gly Gly Leu Val Ile Lys Arg Tyr Leu Glu Ser Arg Ala Pro
274 65           70           75           80
276 tcc tgt gaa acc ctc tcc cat gtc gtc gcc atc ggc tca cct ttg caa      288
277 Ser Cys Glu Thr Leu Ser His Val Val Ala Ile Gly Ser Pro Leu Gln
278           85           90           95
280 gga gct tcc att gtc aat aaa att gag caa tta ggt tta ggg gtg gca      336
281 Gly Ala Ser Ile Val Asn Lys Ile Glu Gln Leu Gly Leu Gly Val Ala
282           100          105          110
284 cta ggt aat tca gca gaa ttt ggg tta aaa gaa cac gac gac gaa tcc      384
285 Leu Gly Asn Ser Ala Glu Phe Gly Leu Lys Glu His Asp Asp Glu Ser
286           115          120          125
288 cgc tat cca caa aaa tca ggc agt att gca gga acg ata cct tta ggg      432
289 Arg Tyr Pro Gln Lys Ser Gly Ser Ile Ala Gly Thr Ile Pro Leu Gly

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290      130      135      140
292 ctg cgc agc ctt tta ctg cgc gat cca ctg gac tcc gat ggt acc gtc      480
293 Leu Arg Ser Leu Leu Leu Arg Asp Pro Leu Asp Ser Asp Gly Thr Val
294 145      150      155      160
296 aca gta gaa gaa acc aaa ata gct ggc atg aca gat cat atc gcg ata      528
297 Thr Val Glu Glu Thr Lys Ile Ala Gly Met Thr Asp His Ile Ala Ile
298      165      170      175
300 tcc acc act tca tac gag aat gct gtt      555
301 Ser Thr Thr Ser Tyr Glu Asn Ala Val
302      180      185
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 185
307 <212> TYPE: PRT
308 <213> ORGANISM: Vibrio metschnikovii RH530
310 <400> SEQUENCE: 5
311 Met Gln Ile Ile Leu Val His Gly Leu Tyr Met His Gly Leu Val Met
312 1 5 10 15
314 His Pro Leu Ser His Arg Leu His Lys Leu Gly Tyr Arg Thr Gln Thr
315 20 25 30
317 Ile Ser Tyr Asn Ser Leu Ala Ile Asp Asp Glu Ala Ile Phe Arg Arg
318 35 40 45
320 Leu Asp Arg Ser Leu Thr His Ala Ser Pro Asn Ala Leu Val Gly His
321 50 55 60
323 Ser Leu Gly Gly Leu Val Ile Lys Arg Tyr Leu Glu Ser Arg Ala Pro
324 65 70 75 80
326 Ser Cys Glu Thr Leu Ser His Val Val Ala Ile Gly Ser Pro Leu Gln
327 85 90 95
329 Gly Ala Ser Ile Val Asn Lys Ile Glu Gln Leu Gly Leu Gly Val Ala
330 100 105 110
332 Leu Gly Asn Ser Ala Glu Phe Gly Leu Lys Glu His Asp Asp Glu Ser
333 115 120 125
335 Arg Tyr Pro Gln Lys Ser Gly Ser Ile Ala Gly Thr Ile Pro Leu Gly
336 130 135 140
338 Leu Arg Ser Leu Leu Leu Arg Asp Pro Leu Asp Ser Asp Gly Thr Val
339 145 150 155 160
341 Thr Val Glu Glu Thr Lys Ile Ala Gly Met Thr Asp His Ile Ala Ile
342 165 170 175
344 Ser Thr Thr Ser Tyr Glu Asn Ala Val
345 180 185
348 <210> SEQ ID NO: 6
349 <211> LENGTH: 117
350 <212> TYPE: PRT
351 <213> ORGANISM: Pseudomonas glumae
353 <400> SEQUENCE: 6
354 Val Ala Asn Leu Ser Gly Phe Gln Ser Asp Asp Gly Pro Asn Gly Arg
355 1 5 10 15
357 Gly Glu Gln Leu Leu Ala Tyr Val Lys Gln Val Leu Ala Thr Thr Gly
358 20 25 30
360 Ala Thr Lys Val Asn Leu Ile Gly His Ser Gln Gly Gly Leu Thr Ser

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VERIFICATION SUMMARY

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L:8 M:270 C: Current Application Number differs, Replaced Current Application No

L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE